

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/234,208D  
Source: 1FW16  
Date Processed by STIC: 12/3/04

# ***ENTERED***



IFW16

RAW SEQUENCE LISTING                      DATE: 12/03/2004  
 PATENT APPLICATION: US/09/234,208D        TIME: 10:26:03

Input Set : A:\09234208 SEQ LIST.txt  
 Output Set: N:\CRF4\12032004\I234208D.raw

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3 <110> APPLICANT: Doherty, Joni Kristin
4   Clinton, Gail M.
6 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
8 <130> FILE REFERENCE: 49321-1
10 <140> CURRENT APPLICATION NUMBER: 09/234,208D
11 <141> CURRENT FILING DATE: 1999-01-20
13 <160> NUMBER OF SEQ ID NOS: 12
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 79
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
24 Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala Val Pro Val Pro Leu
25 1           5           10           15
28 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
29           20           25           30
32 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
33           35           40           45
36 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro
37           50           55           60
40 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly
41 65           70           75
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 419
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 2
51 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
52 1           5           10           15
55 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys
56           20           25           30
59 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
60           35           40           45
63 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
64           50           55           60
67 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
68 65           70           75           80
71 Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu
72           85           90           95
75 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
76           100          105          110
79 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro

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80          115          120          125
83 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
84          130          135          140
87 Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
88 145          150          155          160
91 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
92          165          170          175
95 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
96          180          185          190
99 His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
100          195          200          205
103 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
104          210          215          220
107 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
108 225          230          235          240
111 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
112          245          250          255
115 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
116          260          265          270
119 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg
120          275          280          285
123 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu
124          290          295          300
127 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
128 305          310          315          320
131 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
132          325          330          335
135 Pro Cys Ala Arg Gly Thr His Ser Leu Pro Arg Pro Ala Ala Val
136          340          345          350
139 Pro Val Pro Leu Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser
140          355          360          365
143 Phe Leu Arg Pro Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro
144          370          375          380
147 Leu Ala Pro Leu Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val
148 385          390          395          400
151 Gly Arg Gly Pro Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg
152          405          410          415
155 Tyr Glu Gly

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159 &lt;210&gt; SEQ ID NO: 3

160 &lt;211&gt; LENGTH: 19

161 &lt;212&gt; TYPE: DNA

162 &lt;213&gt; ORGANISM: artificial sequence

164 &lt;220&gt; FEATURE:

165 &lt;223&gt; OTHER INFORMATION: primer

167 &lt;400&gt; SEQUENCE: 3

168 tgagcaccat ggagctggc

171 &lt;210&gt; SEQ ID NO: 4

172 &lt;211&gt; LENGTH: 22

173 &lt;212&gt; TYPE: DNA

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Input Set : A:\09234208 SEQ LIST.txt

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174 <213> ORGANISM: artificial sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: primer
179 <400> SEQUENCE: 4
180 tccggcagaa atgccaggct cc 22
183 <210> SEQ ID NO: 5
184 <211> LENGTH: 22
185 <212> TYPE: DNA
186 <213> ORGANISM: artificial sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: primer
191 <400> SEQUENCE: 5
192 aacacagcgg tgtgagaagt gc 22
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 21
197 <212> TYPE: DNA
198 <213> ORGANISM: artificial sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: primer
203 <400> SEQUENCE: 6
204 ataccgggac aggtcaacag c 21
207 <210> SEQ ID NO: 7
208 <211> LENGTH: 20
209 <212> TYPE: DNA
210 <213> ORGANISM: artificial sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: primer
215 <400> SEQUENCE: 7
216 tctgggtacc cactcactgc 20
219 <210> SEQ ID NO: 8
220 <211> LENGTH: 22
221 <212> TYPE: DNA
222 <213> ORGANISM: artificial sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: primer
227 <400> SEQUENCE: 8
228 ttcacactgg cacgtccaga cc 22
231 <210> SEQ ID NO: 9
232 <211> LENGTH: 27
233 <212> TYPE: DNA
234 <213> ORGANISM: artificial sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: primer
239 <400> SEQUENCE: 9
240 gcacggatcc atagcagact gaggagg 27
243 <210> SEQ ID NO: 10
244 <211> LENGTH: 287
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens

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248 <400> SEQUENCE: 10
249 cccgaggtac ccactcactg ctccccgagge cagctgcagt tcctgtccct ctgcgcgatgc      60
251 agcctggccc agcccaccct gtcctatcct tcctcagacc ctcttggggac ctagtctctg      120
253 ccttctactc tctacccttg gccccctca gcccacaag tgccctata tccccgtca      180
255 gtgtggggag gggcccgac cctgatgctc atgtggctgt taacctgtcc cggtatgaag      240
257 gctgagacgg ccccttcccc caccacccc cacctcctca gtgtgct      287
260 <210> SEQ ID NO: 11
261 <211> LENGTH: 276
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapiens
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(240)
269 <223> OTHER INFORMATION: ECDIIIa intron-encoded region of herstatin
271 <400> SEQUENCE: 11
272 ggt acc cac tca ctg ctc ccg agg cca gct gca gtt cct gtc cct ctg      48
273 Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala Val Pro Val Pro Leu
274 1          5          10          15
276 cgc atg cag cct ggc cca gcc cac cct gtc cta tcc ttc ctc aga ccc      96
277 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
278          20          25          30
280 tct tgg gac cta gtc tct gcc ttc tac tct cta ccc ctg gcc ccc ctc      144
281 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
282          35          40          45
284 agc ccc aca agt gtc cct ata tcc cct gtc agt gtg ggg agg ggc ccg      192
285 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro
286          50          55          60
288 gac cct gat gct cat gtg gct gtt aac ctg tcc cgg tat gaa ggc tga      240
289 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly
290 65          70          75
292 gacggccct tccccaccc accccacct cctcag      276
295 <210> SEQ ID NO: 12
296 <211> LENGTH: 79
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
300 <400> SEQUENCE: 12
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303 1          5          10          15
306 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
307          20          25          30
310 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
311          35          40          45
314 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro
315          50          55          60
318 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly
319 65          70          75

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**VERIFICATION SUMMARY**

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